78655

Access DB# ____________

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: [illegible] Examiner #: [illegible] Date: 10/24/02

Art Unit: [illegible] Phone Number 30 [illegible] Serial Number: 09/737,363

Mail Box and Bldg/Room Location: [illegible] Results Format Preferred (circle): PAPER DISK E-MAIL

[illegible]

If more than one search is submitted, please prioritize searches in order of need.

****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: [illegible]

Inventors (please provide full names): Phillips et al

Earliest Priority Filing Date: 12/12/00

***For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.**

Please search Seq ID Nos:
25, 45, 46, 9, 10, 8,
26, 41, 42, 43

[All seq are less than 10 nt ?]

Please limit to 50 NT.

[illegible]

8-3 41-6
9-6 42-6
10-6 43-6
25-6 45-6
26-6 46 6

Point of Contact:
Thomas G. Larson, Ph.D.
703-308-7309
CM1, Rm. 6 B 01

****

STAFF USE ONLY

Searcher:	Point of Contact: Thomas G. Larson, Ph.D.	NA Sequence (#)	10	STN	
Searcher Phone #:	703-308-7309	AA Sequence (#)		Dialog	
Searcher Location:	CM1, Rm. 6 B 01	Structure (#)		Questel/Orbit	
Date Searcher Picked Up:	10/25	Bibliographic		Dr.Link	
Date Completed:	10/30	Litigation		Lexis/Nexis	
Searcher Prep & Review Time:	60	Fulltext		Sequence Systems	[illegible]
Clerical Prep Time:		Patent Family		WWW/Internet	
Online Time:	30	Other		Other (specify)	

Type of Search / **Vendors and cost where applicable**

PTO-1590 (8-01)

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: October 30, 2002, 08:20:42 ; Search time 635.053 Seconds
(without alignments)
127.520 Million cell updates/sec

Title: US-09-735-363A-45
Perfect score: 6
Sequence: 1 gggagg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 89578

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	6	100.0	6	2	BG927410	Bg927410 HNC1-1-G7
	2	6	100.0	10	9	AW672604	AW672604 11F Expla
c	3	6	100.0	13	10	BM399550	BM399550 5009-0-59
	4	6	100.0	16	9	AA968729	AA968729 or69h11.s
c	5	6	100.0	16	9	AI075064	AI075064 ou61g11.x
c	6	6	100.0	16	9	AI094839	AI094839 qa22c08.x
c	7	6	100.0	16	9	AI274782	AI274782 qv67h03.x
	8	6	100.0	16	9	AI560058	AI560058 tq38h11.x
c	9	6	100.0	16	9	AI569544	AI569544 to28d10.x
	10	6	100.0	18	9	AW250267	AW250267 2821151.5
c	11	6	100.0	18	10	BG896958	BG896958 HOA59-1-D
c	12	6	100.0	18	10	BG925569	BG925569 HNC5-1-E2
c	13	6	100.0	19	9	AA885444	AA885444 am14h07.s
	14	6	100.0	19	9	AA918795	AA918795 ol69c05.s
	15	6	100.0	19	9	AA934650	AA934650 oo71d10.s
c	16	6	100.0	19	9	AI251781	AI251781 qu76g01.x
c	17	6	100.0	19	9	AI360784	AI360784 qx98g07.x
	18	6	100.0	19	9	AI648553	AI648553 tz55e07.x
	19	6	100.0	19	9	AI696833	AI696833 wc74e09.x
c	20	6	100.0	19	9	AI758301	AI758301 ty06a07.x
	21	6	100.0	19	9	AI811474	AI811474 tw43c04.x
	22	6	100.0	19	12	AZ307462	AZ307462 1M0009I08
	23	6	100.0	19	12	AZ324165	AZ324165 1M0046C06
	24	6	100.0	19	12	AZ345792	AZ345792 1M0080G12
	25	6	100.0	19	12	AZ412553	AZ412553 1M0186M03
c	26	6	100.0	19	12	AZ418201	AZ418201 1M0194M12
c	27	6	100.0	19	12	AZ443948	AZ443948 1M0238P04
c	28	6	100.0	19	12	AZ445563	AZ445563 1M0241P18
c	29	6	100.0	19	12	AZ447248	AZ447248 1M0244H23
c	30	6	100.0	19	12	AZ447414	AZ447414 1M0244L06
c	31	6	100.0	19	12	AZ510143	AZ510143 1M0354P21
	32	6	100.0	19	12	AZ512762	AZ512762 1M0358M04
c	33	6	100.0	19	12	AZ579189	AZ579189 1M0363I12
c	34	6	100.0	19	12	AZ595016	AZ595016 1M0407C19
c	35	6	100.0	19	12	AZ597219	AZ597219 1M0411K23
	36	6	100.0	19	12	AZ654214	AZ654214 1M0528H13
	37	6	100.0	19	12	AZ656937	AZ656937 1M0532K13
	38	6	100.0	19	12	AZ759944	AZ759944 1M0553O10
c	39	6	100.0	19	12	AZ760597	AZ760597 1M0554N21
	40	6	100.0	19	12	AZ762504	AZ762504 1M0557M14
c	41	6	100.0	19	12	AZ783420	AZ783420 2M0025D07
	42	6	100.0	19	12	AZ786308	AZ786308 2M0031B17
	43	6	100.0	19	12	AZ807034	AZ807034 2M0069B05
c	44	6	100.0	19	12	AZ835034	AZ835034 2M0129K04
c	45	6	100.0	19	12	AZ842379	AZ842379 2M0140N17

ALIGNMENTS

RESULT 1
BG927410/c
ID BG927410 standard; RNA; EST; 6 BP.
XX
AC BG927410;
XX
SV BG927410.1
XX
DT 09-JUN-2001 (Rel. 68, Created)
DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)
XX
DE HNC1-1-G7.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.
XX
KW EST.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-6
RX MEDLINE; 21482651.
RX PUBMED; 11597177.
RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
RA Sathe G.M., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;
RT "Identification and initial characterization of 5000 expressed sequenced
RT tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA
RT libraries";
RL Osteoarthritis Cartilage 9(7):641-653(2001).
XX
CC Contact: Sanjay Kumar
CC UW2109
CC GlaxoSmithKline
CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
CC Tel: 610-270-7245
CC Fax: 610-270-5598
CC Email: sanjay_kumar-1@gsk.com
CC Seq primer: T7.
XX
FH Key Location/Qualifiers

```
FH
FT   source          1. .6
FT                   /db_xref="taxon:9606"
FT                   /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
FT                   Directional"
FT                   /organism="Homo sapiens"
FT                   /clone_lib="HNC (Human Normal Cartilage)"
FT                   /tissue_type="cartilage"
FT                   /lab_host="E.coli DH10 B"
XX
SQ   Sequence 6 BP; 0 A; 5 C; 0 G; 1 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+09;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      6 GGGAGG 1


RESULT 2
AW672604
LOCUS       AW672604                 10 bp    mRNA    linear   EST 26-SEP-2001
DEFINITION  11F Explanted metanephric mesenchyme induced to differentiate into
            epithelial structures of the nephron ex vivo. Rattus norvegicus
            cDNA similar to similar to: ref|NM_004844.1|| Homo sapiens
            SH3-domain binding protein 5 (BTK-associated) (SH3BP5), mRNA, mRNA
            sequence.
ACCESSION   AW672604
VERSION     AW672604.1  GI:7541084
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Plisov,S.Y., Ivanov,S.V., Yoshino,K., Dove,L.F., Plisova,T.M.,
            Higinbotham,K.G., Karavanova,I., Lerman,M. and Perantoni,A.O.
  TITLE     Mesenchymal-epithelial transition in the developing metanephric
            kidney: gene expression study by differential display
  JOURNAL   Genesis 27 (1), 22-31 (2000)
  MEDLINE   20321327
COMMENT     Contact: Plisov S.Y.
            Laboratory of Comparative Carcinogenesis
            National Cancer Institute
            FCRDC, Bldg.538, Room 205, Frederick, MD 21702, USA
            Tel: 301 846 1242
            Fax: 301 846 4956
            Email: plisov@mail.ncifcrf.gov
            PCR PRimers
            FORWARD: ctcgagatgcacg
            BACKWARD: ttaagctttttttttttc
            Insert Length: 460   Std Error: 0.00
            Seq primer: SP6
            High quality sequence stop: 268
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
                     /clone_lib="Explanted metanephric mesenchyme induced to
                     differentiate into epithelial structures of the nephron ex
                     vivo."
                     /tissue_type="Metanephric mesenchyme"
                     /cell_type="Mesenchymal/Epithelial"
                     /dev_stage="13 dpc-16dpc"
                     /lab_host="JM109"
                     /note="Organ: Kidney; Vector: pGEM-TEasy (Promega).;
                     Restriction Enzymes 1; ApaI, AatII, SphI, NcoI, BstZI,
                     NotI, SacII, and EcoRI SpeI, EcoRI, NotI, BstZI, PstI,
                     SalI, NdeI, SacI, BstXI, and NsiI cDNA fragment
                     PCR-amplified in mRNA differential display analysis;
                     cloned in pGEM-TEasy (Promega); its expression is
                     developmentally  regulated during mesenchymal-epithelial
                     conversion in the metanephric kidney."
BASE COUNT        1 a      0 c      9 g      0 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      1 GGGAGG 6


RESULT 3
BM399550/c
LOCUS       BM399550                 13 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-59-C05.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM399550
VERSION     BM399550.1  GI:18199603
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila.
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
            ,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Tetrahymena thermophila"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT        0 a      6 c      5 g      2 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 10;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      6 GGGAGG 1


RESULT 4
AA968729
LOCUS       AA968729                 16 bp    mRNA    linear   EST 27-AUG-1998
DEFINITION  or69h11.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1601157 3'
            similar to SW:PRPE_HUMAN P02811 BASIC PROLINE-RICH PEPTIDE P-E
            ;contains element MSR1 repetitive element ;, mRNA sequence.
ACCESSION   AA968729
VERSION     AA968729.1  GI:3143909
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 514    Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1601157"
                      /clone_lib="NCI_CGAP_GC3"
                      /tissue_type="pooled germ cell tumors"
                      /lab_host="DH10B"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; 1st strand cDNA was prepared from 3 pooled
                      germ cell tumors, and was then primed with a Not I -
                      oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                      RI adaptors (Pharmacia), digested with Not I and cloned
                      into the Not I and Eco RI sites of the modified pT7T3
                      vector.  Library is not normalized. Library was
                      constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT        2 a      1 c     13 g      0 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 9;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGAGG 6
           ||||||
Db       5 GGGAGG 10


RESULT 5
AI075064/c
LOCUS       AI075064                  16 bp    mRNA    linear   EST 27-AUG-1998
DEFINITION  ou61g11.x1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632356 3'
            similar to TR:Q24348 Q24348 FIBRILLARIN ;, mRNA sequence.
ACCESSION   AI075064
VERSION     AI075064.1  GI:3399844
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 712    Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1632356"
                      /clone_lib="NCI_CGAP_Br2"
                      /sex="female, pooled"
                      /tissue_type="breast"
                      /lab_host="DH10B"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; 1st strand cDNA was prepared from pooled bulk
                      breast tumor tissue, and was then primed with a Not I -
                      oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                      RI adaptors (Pharmacia), digested with Not I and cloned
                      into the Not I and Eco RI sites of the modified pT7T3
                      vector.  This library is the normalized version of
                      NCI_CGAP_Br1.1. Library was constructed by Bento Soares
                      and M. Fatima Bonaldo. "
BASE COUNT        0 a     12 c      0 g      4 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 9;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGAGG 6
           ||||||
Db       8 GGGAGG 3


RESULT 6
AI094839/c
LOCUS       AI094839                  16 bp    mRNA    linear   EST 18-AUG-1998
DEFINITION  qa22c08.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1687502 3'
            similar to TR:O00599 O00599 CON1. ;contains element MSR1 repetitive
            element ;, mRNA sequence.
ACCESSION   AI094839
VERSION     AI094839.1  GI:3433815
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGAP), Tumor Gene Index
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .16
```

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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1687502"
                     /clone_lib="NCI_CGAP_Brn23"
                     /tissue_type="glioblastoma (pooled)"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATATCTTTTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     Library is normalized, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT        3 a      9 c      3 g      1 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 9;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db     10 GGGAGG 5


RESULT 7
AI274782/c
LOCUS       AI274782                 16 bp    mRNA    linear   EST 21-DEC-1998
DEFINITION  qv67h03.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:1986677 3'
            similar to WP:F59E12.9 CE11534 ;contains element MSR1 repetitive
            element ;, mRNA sequence.
ACCESSION   AI274782
VERSION     AI274782.1  GI:3897056
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 1556   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1986677"
                     /clone_lib="NCI_CGAP_Ut1"
                     /tissue_type="well-differentiated endometrial
                     adenocarcinoma, 7 pooled tumors"
                     /lab_host="DH10B"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb. Life Technologies catalog #:
                     11538-014"
BASE COUNT        0 a     13 c      2 g      1 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 9;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db     10 GGGAGG 5


RESULT 8
AI560058
LOCUS       AI560058                 16 bp    mRNA    linear   EST 13-MAY-1999
DEFINITION  tq38h11.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2211141 3'
            similar to TR:Q04154 Q04154 SALIVARY PROLINE-RICH PROTEIN RP15
            PRECURSOR. ;contains MSR1.t2 MSR1 repetitive element ;, mRNA
            sequence.
ACCESSION   AI560058
VERSION     AI560058.1  GI:4510263
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 2104   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2211141"
                     /clone_lib="NCI_CGAP_Ut1"
                     /tissue_type="well-differentiated endometrial
                     adenocarcinoma, 7 pooled tumors"
                     /lab_host="DH10B"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb. Life Technologies catalog #:
                     11538-014"
BASE COUNT        1 a      4 c     11 g      0 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 9;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      8 GGGAGG 13


RESULT 9
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AI569544/c
LOCUS       AI569544                 16 bp    mRNA    linear   EST 12-MAY-1999
DEFINITION  to28d10.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2180371 3'
            similar to TR:Q18444 Q18444 COSMID C34D4. ;contains MSR1.b2 MSR1
            repetitive element ;, mRNA sequence.
ACCESSION   AI569544
VERSION     AI569544.1  GI:4532918
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 1683   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2180371"
                     /clone_lib="NCI_CGAP_Ut4"
                     /tissue_type="serous papillary carcinoma, high grade, 2
                     pooled tumors"
                     /lab_host="DH10B"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.48 kb. Life Technologies catalog #:
                     11542-016"
BASE COUNT        1 a     14 c      0 g      1 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 9;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      8 GGGAGG 3


RESULT 10
AW250267
LOCUS       AW250267                 18 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2821151.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821151 5',
            mRNA sequence.
ACCESSION   AW250267
VERSION     AW250267.1  GI:6593260
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2821151.3prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 16
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 18 contiguous distinct
            peaks following vector sequence.
            Plate: LLCM6  row: A  column: 24
            High quality sequence stop: 16.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821151"
                     /clone_lib="NIH_MGC_7"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT        3 a      3 c     12 g      0 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 9;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      9 GGGAGG 14


RESULT 11
BG896958/c
LOCUS       BG896958                 18 bp    mRNA    linear   EST 06-NOV-2001
DEFINITION  HOA59-1-D4.R HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA
            , mRNA sequence.
ACCESSION   BG896958
VERSION     BG896958.1  GI:14307199
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
            Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
            Lark,M.W.
  TITLE     Identification and initial characterization of 5000 expressed
            sequenced tags (ESTs) each from adult human normal and
            osteoarthritic cartilage cDNA libraries
  JOURNAL   Osteoarthritis Cartilage 9 (7), 641-653 (2001)
  MEDLINE   21482651
COMMENT     Contact: Sanjay Kumar
            UW2109
            GlaxoSmithKline
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            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay_kumar-1@gsk.com
            Seq primer: T7.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone_lib="HOA (Human Osteoarthritic Cartilage)"
                      /tissue_type="cartilage"
                      /lab_host="E.coli DH10 B"
                      /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
                      Directional"
BASE COUNT        1 a     11 c      0 g      6 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 10;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db     11 GGGAGG 6


RESULT 12
BG925569/c
LOCUS       BG925569                 18 bp    mRNA    linear   EST 06-NOV-2001
DEFINITION  HNC5-1-E2.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   BG925569
VERSION     BG925569.1  GI:14320092
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
            Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
            Lark,M.W.
  TITLE     Identification and initial characterization of 5000 expressed
            sequenced tags (ESTs) each from adult human normal and
            osteoarthritic cartilage cDNA libraries
  JOURNAL   Osteoarthritis Cartilage 9 (7), 641-653 (2001)
  MEDLINE   21482651
COMMENT     Contact: Sanjay Kumar
            UW2109
            GlaxoSmithKline
            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay_kumar-1@gsk.com
            Seq primer: T7.
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone_lib="HNC (Human Normal Cartilage)"
                      /tissue_type="cartilage"
                      /lab_host="E.coli DH10 B"
                      /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
                      Directional"
BASE COUNT        1 a     12 c      0 g      5 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 10;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      8 GGGAGG 3


RESULT 13
AA885444/c
LOCUS       AA885444                 19 bp    mRNA    linear   EST 04-JAN-1999
DEFINITION  am14h07.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:1466845 3' similar to TR:O00409 O00409 CHECKPOINT SUPPRESSOR
            1. ;, mRNA sequence.
ACCESSION   AA885444
VERSION     AA885444.1  GI:2994521
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Insert Length: 489   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1466845"
                      /clone_lib="Soares_NFL_T_GBC_S1"
                      /lab_host="DH10B"
                      /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                      a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                      Equal amounts of plasmid DNA from three normalized
                      libraries (fetal lung NbHL19W, testis NHT, and B-cell
                      NCI_CGAP_GCB1) were mixed, and ss circles were made in
                      vitro. Following HAP purification, this DNA was used as
                      tracer in a subtractive hybridization reaction. The driver
                      was PCR-amplified cDNAs from pools of 5,000 clones made
                      from the same 3 libraries. The pools consisted of
                      I.M.A.G.E. clones 297480-302087, 682632-687239,
                      726408-728711, and 729096-731399. Subtraction by Bento
                      Soares and M. Fatima Bonaldo.  "
BASE COUNT        2 a      8 c      5 g      4 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 9;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db     19 GGGAGG 14


RESULT 14
AA918795
LOCUS       AA918795                 19 bp    mRNA    linear   EST 10-JUN-1998
DEFINITION  ol69c05.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1534856 3'
            similar to TR:Q39599 Q39599 EXTENSIN. ;contains TAR1.b2 TAR1
            repetitive element ;, mRNA sequence.
ACCESSION   AA918795
VERSION     AA918795.1  GI:3058685
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 814   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES                Location/Qualifiers
     source             1. .19
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:1534856"
                        /clone_lib="NCI_CGAP_Kid3"
                        /lab_host="DH10B"
                        /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                        a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                        strand cDNA was primed with a Not I - oligo(dT) primer,
                        double-stranded cDNA was ligated to Eco RI adaptors
                        (Pharmacia), digested with Not I and cloned into the Not
                        I and Eco RI sites of the modified pT7T3 vector. mRNA
                        source: 2 pooled kidneys. Library went through one round
                        of normalization. Library constructed by Bento Soares and
                        M. Fatima Bonaldo. "
BASE COUNT        3 a      0 c     16 g      0 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 9;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGAGG 6
           ||||||
Db      11 GGGAGG 16


RESULT 15
AA934650
LOCUS       AA934650                 19 bp    mRNA    linear   EST 28-APR-1998
DEFINITION  oo71d10.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571635 3'
            similar to TR:O15047 O15047 KIAA0339. ;, mRNA sequence.
ACCESSION   AA934650
VERSION     AA934650.1  GI:3091862
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES                Location/Qualifiers
     source             1. .19
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:1571635"
                        /clone_lib="NCI_CGAP_GC4"
                        /tissue_type="pooled germ cell tumors"
                        /lab_host="DH10B"
                        /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                        polylinker; 1st strand cDNA was prepared from 3 pooled
                        germ cell tumors, and was then primed with a Not I -
                        oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                        RI adaptors (Pharmacia), digested with Not I and cloned
                        into the Not I and Eco RI sites of the modified pT7T3
                        vector.  Library is normalized. Library was constructed by
                        Bento Soares and M. Fatima Bonaldo. "
BASE COUNT        1 a      4 c     11 g      3 t
ORIGIN

  Query Match             100.0%;  Score 6;  DB 9;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGAGG 6
           ||||||
Db       2 GGGAGG 7


Search completed: October 30, 2002, 10:42:09
Job time : 637.053 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: October 29, 2002, 17:58:36 ; Search time 335.474 Seconds
(without alignments)
374.274 Million cell updates/sec

Title: US-09-735-363A-45
Perfect score: 6
Sequence: 1 gggagg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 708260

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	6	100.0	6	6	AX175281	AX175281 Sequence
c	2	6	100.0	8	6	AX286327	AX286327 Sequence
c	3	6	100.0	9	6	A70954	A70954 Sequence 8
	4	6	100.0	9	6	AX103813	AX103813 Sequence
	5	6	100.0	9	6	AX103814	AX103814 Sequence
	6	6	100.0	9	6	AX214433	AX214433 Sequence
	7	6	100.0	9	6	AX319721	AX319721 Sequence
c	8	6	100.0	9	6	AX319722	AX319722 Sequence
	9	6	100.0	9	6	AX320671	AX320671 Sequence
	10	6	100.0	9	6	AX355391	AX355391 Sequence
	11	6	100.0	9	6	AX355392	AX355392 Sequence
	12	6	100.0	10	6	AR030218	AR030218 Sequence
	13	6	100.0	10	6	AR058519	AR058519 Sequence
c	14	6	100.0	10	6	AR058771	AR058771 Sequence
c	15	6	100.0	10	6	AR058772	AR058772 Sequence
c	16	6	100.0	10	6	AR058773	AR058773 Sequence
c	17	6	100.0	10	6	AR058774	AR058774 Sequence
c	18	6	100.0	10	6	AX152136	AX152136 Sequence
c	19	6	100.0	10	6	AX152183	AX152183 Sequence
c	20	6	100.0	10	6	AX152246	AX152246 Sequence
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	23	6	100.0	10	6	AX152421	AX152421 Sequence
c	24	6	100.0	10	6	AX152726	AX152726 Sequence
c	25	6	100.0	10	6	AX152747	AX152747 Sequence
c	26	6	100.0	10	6	AX152940	AX152940 Sequence
	27	6	100.0	10	6	AX152946	AX152946 Sequence
c	28	6	100.0	10	6	AX153046	AX153046 Sequence
c	29	6	100.0	10	6	AX153160	AX153160 Sequence
c	30	6	100.0	10	6	AX153189	AX153189 Sequence
c	31	6	100.0	10	6	AX301481	AX301481 Sequence
c	32	6	100.0	10	6	AX301502	AX301502 Sequence
c	33	6	100.0	10	6	AX301503	AX301503 Sequence
c	34	6	100.0	10	6	AX301724	AX301724 Sequence
	35	6	100.0	10	6	AX302573	AX302573 Sequence
	36	6	100.0	10	6	AX302593	AX302593 Sequence
	37	6	100.0	10	6	AX319696	AX319696 Sequence
	38	6	100.0	10	6	E05324	E05324 Anti-sense
c	39	6	100.0	10	6	I17723	I17723 Sequence 3
c	40	6	100.0	11	6	A70952	A70952 Sequence 6
c	41	6	100.0	11	6	AR029861	AR029861 Sequence
c	42	6	100.0	11	6	AR029864	AR029864 Sequence
c	43	6	100.0	11	6	AR029865	AR029865 Sequence
c	44	6	100.0	11	6	AR029932	AR029932 Sequence
c	45	6	100.0	11	6	AR029933	AR029933 Sequence

ALIGNMENTS

RESULT 1
AX175281
LOCUS AX175281 6 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 45 from Patent WO0144465.
ACCESSION AX175281
VERSION AX175281.1 GI:14598649
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 6)
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 45 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES Location/Qualifiers
source 1. .6
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 1 a 0 c 5 g 0 t
ORIGIN

Query Match 100.0%; Score 6; DB 6; Length 6;

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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      1 GGGAGG 6


RESULT 2
AX286327/c
LOCUS       AX286327                  8 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 6 from Patent WO0181591.
ACCESSION   AX286327
VERSION     AX286327.1  GI:17048574
KEYWORDS    .
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (sites)
  AUTHORS   Boisson,M., Gomord,V., Lerouge,P., Faye,L., Caboche,M. and
            Lepiniec,L.
  TITLE     Novel plant glucosidase i and use thereof for producing recombinant
            proteins with modified glycosylation
  JOURNAL   Patent: WO 0181591-A 6 01-NOV-2001;
            INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ; CENTRE
            NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES             Location/Qualifiers
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                     /organism="Arabidopsis thaliana"
                     /db_xref="taxon:3702"
     misc_feature    1
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                     sucre"
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                     /note="Groupe amino en position 3' du sucre"
BASE COUNT        1 a      6 c      0 g      1 t
ORIGIN

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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      7 GGGAGG 2


RESULT 3
A70954/c
LOCUS       A70954                    9 bp    DNA     linear   PAT 07-MAY-1999
DEFINITION  Sequence 8 from Patent WO9813522.
ACCESSION   A70954
VERSION     A70954.1  GI:4774939
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Uhlen,M. and Lundeberg,J.
  TITLE     THE USE OF MODULAR OLIGONUCLEOTIDES AS PROBES OR PRIMERS IN NUCLEIC
            ACID BASED ASSAY
  JOURNAL   Patent: WO 9813522-A 8 02-APR-1998;
            DZIEGLEWSKA HANNA EVA (GB)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        0 a      5 c      3 g      1 t
ORIGIN

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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
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Db      6 GGGAGG 1


RESULT 4
AX103813
LOCUS       AX103813                  9 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 5 from Patent WO0122972.
ACCESSION   AX103813
VERSION     AX103813.1  GI:13920010
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 5 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .9
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BASE COUNT        1 a      0 c      7 g      1 t
ORIGIN

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Qy      1 GGGAGG 6
          ||||||
Db      2 GGGAGG 7


RESULT 5
AX103814
LOCUS       AX103814                  9 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 6 from Patent WO0122972.
ACCESSION   AX103814
VERSION     AX103814.1  GI:13920011
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 6 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
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BASE COUNT        1 a      0 c      8 g      0 t
ORIGIN

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Qy      1 GGGAGG 6
          ||||||
Db      2 GGGAGG 7


RESULT 6
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AX214433
LOCUS       AX214433                  9 bp    DNA     linear   PAT 06-SEP-2001
DEFINITION  Sequence 41 from Patent WO0159450.
ACCESSION   AX214433
VERSION     AX214433.1  GI:15524493
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Case,C.
  TITLE     Cells for drug discovery
  JOURNAL   Patent: WO 0159450-A 41 16-AUG-2001;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
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                     /note="target sequence"
BASE COUNT        1 a      1 c      7 g      0 t
ORIGIN

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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      2 GGGAGG 7


RESULT 7
AX319721
LOCUS       AX319721                  9 bp    DNA     linear   PAT 14-DEC-2001
DEFINITION  Sequence 27 from Patent WO0183751.
ACCESSION   AX319721
VERSION     AX319721.1  GI:17901362
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (sites)
  AUTHORS   Raschke,E., Wolffe,A.P. and Case,C.C.
  TITLE     Methods for binding an exogenous molecule to cellular chromatin
  JOURNAL   Patent: WO 0183751-A 27 08-NOV-2001;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
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                     /db_xref="taxon:32630"
                     /note="target sequence 3"
BASE COUNT        2 a      0 c      7 g      0 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 2.3e+09;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      2 GGGAGG 7


RESULT 8
AX319722/c
LOCUS       AX319722                  9 bp    DNA     linear   PAT 14-DEC-2001
DEFINITION  Sequence 28 from Patent WO0183751.
ACCESSION   AX319722
VERSION     AX319722.1  GI:17901363
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (sites)
  AUTHORS   Raschke,E., Wolffe,A.P. and Case,C.C.
  TITLE     Methods for binding an exogenous molecule to cellular chromatin
  JOURNAL   Patent: WO 0183751-A 28 08-NOV-2001;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
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                     /db_xref="taxon:32630"
                     /note="sequence complementary to target sequence 3"
BASE COUNT        0 a      7 c      0 g      2 t
ORIGIN

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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      8 GGGAGG 3


RESULT 9
AX320671
LOCUS       AX320671                  9 bp    DNA     linear   PAT 14-DEC-2001
DEFINITION  Sequence 2 from Patent WO0183793.
ACCESSION   AX320671
VERSION     AX320671.1  GI:17902330
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (sites)
  AUTHORS   Wolffe,A.P. and Collingwood,T.
  TITLE     Targeted modification of chromatin structure
  JOURNAL   Patent: WO 0183793-A 2 08-NOV-2001;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
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ORIGIN

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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      2 GGGAGG 7


RESULT 10
AX355391
LOCUS       AX355391                  9 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 419 from Patent WO0197843.
ACCESSION   AX355391
VERSION     AX355391.1  GI:18620059
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (sites)
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 419 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      2 GGGAGG 7


RESULT 11
AX355392
LOCUS       AX355392                   9 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 420 from Patent WO0197843.
ACCESSION   AX355392
VERSION     AX355392.1  GI:18620060
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (sites)
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 420 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
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                     /note="Synthetic oligonucleotide-phosphorothioate
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BASE COUNT        1 a      0 c      7 g      1 t
ORIGIN

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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      2 GGGAGG 7


RESULT 12
AR030218
LOCUS       AR030218                  10 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 29 from patent US 5861246.
ACCESSION   AR030218
VERSION     AR030218.1  GI:5943432
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Weissman,S.M., Nallur,G.N. and Kulkarni,P.
  TITLE     Multiple selection process for binding sites of DNA-binding
            proteins
  JOURNAL   Patent: US 5861246-A 29 19-JAN-1999;
FEATURES             Location/Qualifiers
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BASE COUNT        1 a      0 c      7 g      2 t
ORIGIN

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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      3 GGGAGG 8


RESULT 13
AR058519
LOCUS       AR058519                  10 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 96 from patent US 5837832.
ACCESSION   AR058519
VERSION     AR058519.1  GI:5984096
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
            Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
  TITLE     Arrays of nucleic acid probes on biological chips
  JOURNAL   Patent: US 5837832-A 96 17-NOV-1998;
FEATURES             Location/Qualifiers
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BASE COUNT        1 a      1 c      8 g      0 t
ORIGIN

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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      5 GGGAGG 10


RESULT 14
AR058771/c
LOCUS       AR058771                  10 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 348 from patent US 5837832.
ACCESSION   AR058771
VERSION     AR058771.1  GI:5984348
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
            Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
  TITLE     Arrays of nucleic acid probes on biological chips
  JOURNAL   Patent: US 5837832-A 348 17-NOV-1998;
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      7 GGGAGG 2


RESULT 15
AR058772/c
LOCUS       AR058772                  10 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 349 from patent US 5837832.
ACCESSION   AR058772
VERSION     AR058772.1  GI:5984349
KEYWORDS    .
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
            Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
  TITLE     Arrays of nucleic acid probes on biological chips
  JOURNAL   Patent: US 5837832-A 349 17-NOV-1998;
FEATURES             Location/Qualifiers
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BASE COUNT        0 a      7 c      1 g      2 t
ORIGIN

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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGAGG 6
           ||||||
Db       8 GGGAGG 3


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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

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97.910 Million cell updates/sec

Title: US-09-735-363A-45
Perfect score: 6
Sequence: 1 gggagg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	6	100.0	8	1	US-08-187-749-11	Sequence 11, Appl
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	3	6	100.0	8	3	US-09-069-434-12	Sequence 12, Appl
	4	6	100.0	8	3	US-09-069-434-13	Sequence 13, Appl
	5	6	100.0	8	5	PCT-US95-01104-11	Sequence 11, Appl
c	6	6	100.0	9	2	US-08-605-163-6	Sequence 6, Appli
c	7	6	100.0	10	1	US-07-963-723A-3	Sequence 3, Appli
	8	6	100.0	10	2	US-08-441-887A-96	Sequence 96, Appl
c	9	6	100.0	10	2	US-08-441-887A-348	Sequence 348, App
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c	11	6	100.0	10	2	US-08-441-887A-350	Sequence 350, App
c	12	6	100.0	10	2	US-08-441-887A-351	Sequence 351, App
	13	6	100.0	10	2	US-08-590-571-29	Sequence 29, Appl
	14	6	100.0	10	3	US-08-906-691-19	Sequence 19, Appl
c	15	6	100.0	10	5	PCT-US93-10072-3	Sequence 3, Appli
c	16	6	100.0	11	1	US-08-233-030-60	Sequence 60, Appl
	17	6	100.0	11	2	US-08-441-887A-39	Sequence 39, Appl
	18	6	100.0	11	2	US-08-441-887A-58	Sequence 58, Appl
	19	6	100.0	11	2	US-08-441-887A-228	Sequence 228, App
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c	21	6	100.0	11	2	US-08-173-489C-53	Sequence 53, Appl
c	22	6	100.0	11	2	US-08-173-489C-54	Sequence 54, Appl
c	23	6	100.0	11	2	US-08-173-489C-121	Sequence 121, App
c	24	6	100.0	11	2	US-08-173-489C-122	Sequence 122, App
	25	6	100.0	11	2	US-08-173-489C-133	Sequence 133, App
c	26	6	100.0	11	2	US-08-173-489C-150	Sequence 150, App
c	27	6	100.0	11	2	US-08-173-489C-159	Sequence 159, App
	28	6	100.0	11	2	US-08-173-489C-195	Sequence 195, App
	29	6	100.0	11	4	US-09-009-490A-95	Sequence 95, Appl
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c	31	6	100.0	12	1	US-08-149-199-12	Sequence 12, Appl
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	36	6	100.0	12	1	US-08-408-656-3	Sequence 3, Appli
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c	38	6	100.0	12	2	US-08-858-767-12	Sequence 12, Appl
c	39	6	100.0	12	2	US-08-441-887A-335	Sequence 335, App
c	40	6	100.0	12	2	US-08-441-887A-336	Sequence 336, App
c	41	6	100.0	12	2	US-08-441-887A-337	Sequence 337, App
c	42	6	100.0	12	2	US-08-441-887A-338	Sequence 338, App
c	43	6	100.0	12	2	US-08-441-887A-339	Sequence 339, App
c	44	6	100.0	12	2	US-08-863-028-10	Sequence 10, Appl
c	45	6	100.0	12	2	US-08-863-028-12	Sequence 12, Appl

ALIGNMENTS

```
RESULT 1
US-08-187-749-11
; Sequence 11, Application US/08187749
; Patent No. 5525470
;  GENERAL INFORMATION:
;    APPLICANT:  Cohen, S. Aharon,
;    APPLICANT:  Belenky, Alexei and
;    APPLICANT:  Ott, Christopher M.
;    TITLE OF INVENTION:  DNA Sequencing Using
;    TITLE OF INVENTION:  High Pressure Capillary
;    TITLE OF INVENTION:  Electrophoresis
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lappin & Kusmer
;      STREET:  200 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/187,749
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kerner, Ann-Louise
;      REGISTRATION NUMBER:  33,523
;      REFERENCE/DOCKET NUMBER:  HYZ-013
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-330-1300
;      TELEFAX:  617-330-1311
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-187-749-11

  Query Match           100.0%;  Score 6;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 2.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy      1 GGGAGG 6
          ||||||
Db      1 GGGAGG 6


RESULT 2
US-09-069-434-11
; Sequence 11, Application US/09069434
; Patent No. 6017709
;  GENERAL INFORMATION:
;    APPLICANT:  HARDIN, Susan H.
;    APPLICANT:  YING, Jun
;    APPLICANT:  JONES, Leslie Burgan
;    TITLE OF INVENTION:  DNA Replication Templates Stabilized by
;    TITLE OF INVENTION:  Guanine Quartets
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/069,434
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DAVIDSON, Ross E.
;      REGISTRATION NUMBER:  P-41,698
;      REFERENCE/DOCKET NUMBER:  P-01480US0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5144
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Oligonucleotide"
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-09-069-434-11

  Query Match             100.0%;  Score 6;  DB 3;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      3 GGGAGG 8


RESULT 3
US-09-069-434-12
; Sequence 12, Application US/09069434
; Patent No. 6017709
;  GENERAL INFORMATION:
;    APPLICANT:  HARDIN, Susan H.
;    APPLICANT:  YING, Jun
;    APPLICANT:  JONES, Leslie Burgan
;    TITLE OF INVENTION:  DNA Replication Templates Stabilized by
;    TITLE OF INVENTION:  Guanine Quartets
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/069,434
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DAVIDSON, Ross E.
;      REGISTRATION NUMBER:  P-41,698
;      REFERENCE/DOCKET NUMBER:  P-01480US0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5144
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Oligonucleotide"
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-09-069-434-12

  Query Match             100.0%;  Score 6;  DB 3;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      2 GGGAGG 7


RESULT 4
US-09-069-434-13
; Sequence 13, Application US/09069434
; Patent No. 6017709
;  GENERAL INFORMATION:
;    APPLICANT:  HARDIN, Susan H.
;    APPLICANT:  YING, Jun
;    APPLICANT:  JONES, Leslie Burgan
;    TITLE OF INVENTION:  DNA Replication Templates Stabilized by
;    TITLE OF INVENTION:  Guanine Quartets
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/069,434
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DAVIDSON, Ross E.
;      REGISTRATION NUMBER:  P-41,698
;      REFERENCE/DOCKET NUMBER:  P-01480US0
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5144
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Oligonucleotide"
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-09-069-434-13

  Query Match           100.0%;  Score 6;  DB 3;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 2.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      1 GGGAGG 6


RESULT 5
PCT-US95-01104-11
; Sequence 11, Application PC/TUS9501104
;  GENERAL INFORMATION:
;    APPLICANT:  Cohen, S. Aharon,
;    APPLICANT:  Belenky, Alexei and
;    APPLICANT:  Ott, Christopher M.
;    TITLE OF INVENTION:  A Method of Sequencing
;    TITLE OF INVENTION:  Short Oligonucleotides
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lappin & Kusmer
;      STREET:  200 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01104
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kerner, Ann-Louise
;      REGISTRATION NUMBER:  33,523
;      REFERENCE/DOCKET NUMBER:  HYZ-013PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-330-1300
;      TELEFAX:  617-330-1311
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
PCT-US95-01104-11

  Query Match           100.0%;  Score 6;  DB 5;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 2.8e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      1 GGGAGG 6


RESULT 6
US-08-605-163-6/c
; Sequence 6, Application US/08605163
; Patent No. 5879886
;  GENERAL INFORMATION:
;    APPLICANT:  Meo, Tommaso
;    APPLICANT:  Tosi, Mario
;    APPLICANT:  Verpy, Elisabeth
;    APPLICANT:  Biasotto, Michel
;    TITLE OF INVENTION:  Method for Detecting Molecules
;    TITLE OF INVENTION:  Containing Nucleotide Mismatches and the Location of These
;    TITLE OF INVENTION:  Mismatches, and Application to the Detection of Base
;    TITLE OF INVENTION:  Substitutions or Deletions in Nucleotide Sequences.
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/605,163
;      FILING DATE:  08-MAR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  05986.0005-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-605-163-6

  Query Match           100.0%;  Score 6;  DB 2;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 2.5e+07;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      7 GGGAGG 2


RESULT 7
US-07-963-723A-3/c
; Sequence 3, Application US/07963723A
; Patent No. 5494794
;  GENERAL INFORMATION:
;    APPLICANT:  Wallace, Douglas C.
;    TITLE OF INVENTION:  Detection of Mitochondrial DNA Mutations
;    TITLE OF INVENTION:  Associated with Alzheimer's Disease and Parkinson's
;    TITLE OF INVENTION:  Disease
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Needle & Rosenberg, P.C.
;      STREET:  133 Carnegie Way, N.W., Suite 400
```

```
;       CITY:  Atlanta
;       STATE:  Georgia
;       COUNTRY:  U.S.A.
;       ZIP:  30301
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/963,723A
;       FILING DATE:  19921020
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Perryman, David G.
;       REGISTRATION NUMBER:  33,438
;       REFERENCE/DOCKET NUMBER:  0510.027
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (404) 688-0770
;       TELEFAX:  (404) 688-9880
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-07-963-723A-3

  Query Match             100.0%;  Score 6;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+04;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGAGG 6
           ||||||
Db       9 GGGAGG 4


RESULT 8
US-08-441-887A-96
; Sequence 96, Application US/08441887A
; Patent No. 5837832
;  GENERAL INFORMATION:
;     APPLICANT:  Chee, Mark
;     APPLICANT:  Cronin, Maureen T.
;     APPLICANT:  Fodor, Stephen P.A.
;     APPLICANT:  Huang, Xiaohua X.
;     APPLICANT:  Hubbell, Earl A.
;     APPLICANT:  Lipshutz, Robert J.
;     APPLICANT:  Lobban, Peter E.
;     APPLICANT:  Morris, Macdonald S.
;     APPLICANT:  Sheldon, Edward L.
;     TITLE OF INVENTION:  Arrays of Nucleic Acid Probes on
;     TITLE OF INVENTION:  Biological Chips
;     NUMBER OF SEQUENCES:  360
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend and Crew LLP
;       STREET:  Two Embarcadero Center, 8th Floor
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94111
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/441,887A
;       FILING DATE:  16-MAY-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/143,312
;       FILING DATE:  26-OCT-1993
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/082,937
;       FILING DATE:  25-JUN-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Liebeschuetz, Joseph O.
;       REGISTRATION NUMBER:  37,505
;       REFERENCE/DOCKET NUMBER:  018547-004160US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650-326-2400
;       TELEFAX:  650-326-2422
;   INFORMATION FOR SEQ ID NO:  96:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (probe)
US-08-441-887A-96

  Query Match             100.0%;  Score 6;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+04;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGAGG 6
           ||||||
Db       5 GGGAGG 10


RESULT 9
US-08-441-887A-348/c
; Sequence 348, Application US/08441887A
; Patent No. 5837832
;  GENERAL INFORMATION:
;     APPLICANT:  Chee, Mark
;     APPLICANT:  Cronin, Maureen T.
;     APPLICANT:  Fodor, Stephen P.A.
;     APPLICANT:  Huang, Xiaohua X.
;     APPLICANT:  Hubbell, Earl A.
;     APPLICANT:  Lipshutz, Robert J.
;     APPLICANT:  Lobban, Peter E.
;     APPLICANT:  Morris, Macdonald S.
;     APPLICANT:  Sheldon, Edward L.
;     TITLE OF INVENTION:  Arrays of Nucleic Acid Probes on
;     TITLE OF INVENTION:  Biological Chips
;     NUMBER OF SEQUENCES:  360
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend and Crew LLP
;       STREET:  Two Embarcadero Center, 8th Floor
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94111
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/441,887A
;       FILING DATE:  16-MAY-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/143,312
;       FILING DATE:  26-OCT-1993
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/082,937
;       FILING DATE:  25-JUN-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Liebeschuetz, Joseph O.
;       REGISTRATION NUMBER:  37,505
```

```
;      REFERENCE/DOCKET NUMBER:  018547-004160US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-326-2400
;      TELEFAX:  650-326-2422
;  INFORMATION FOR SEQ ID NO:  348:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (probe)
US-08-441-887A-348

  Query Match             100.0%;  Score 6;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+04;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      7 GGGAGG 2


RESULT 10
US-08-441-887A-349/c
; Sequence 349, Application US/08441887A
; Patent No. 5837832
;  GENERAL INFORMATION:
;    APPLICANT:  Chee, Mark
;    APPLICANT:  Cronin, Maureen T.
;    APPLICANT:  Fodor, Stephen P.A.
;    APPLICANT:  Huang, Xiaohua X.
;    APPLICANT:  Hubbell, Earl A.
;    APPLICANT:  Lipshutz, Robert J.
;    APPLICANT:  Lobban, Peter E.
;    APPLICANT:  Morris, Macdonald S.
;    APPLICANT:  Sheldon, Edward L.
;    TITLE OF INVENTION:  Arrays of Nucleic Acid Probes on
;    TITLE OF INVENTION:  Biological Chips
;    NUMBER OF SEQUENCES:  360
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/441,887A
;      FILING DATE:  16-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/143,312
;      FILING DATE:  26-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/082,937
;      FILING DATE:  25-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Liebeschuetz, Joseph O.
;      REGISTRATION NUMBER:  37,505
;      REFERENCE/DOCKET NUMBER:  018547-004160US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-326-2400
;      TELEFAX:  650-326-2422
;  INFORMATION FOR SEQ ID NO:  349:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (probe)
US-08-441-887A-349

  Query Match             100.0%;  Score 6;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+04;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      8 GGGAGG 3


RESULT 11
US-08-441-887A-350/c
; Sequence 350, Application US/08441887A
; Patent No. 5837832
;  GENERAL INFORMATION:
;    APPLICANT:  Chee, Mark
;    APPLICANT:  Cronin, Maureen T.
;    APPLICANT:  Fodor, Stephen P.A.
;    APPLICANT:  Huang, Xiaohua X.
;    APPLICANT:  Hubbell, Earl A.
;    APPLICANT:  Lipshutz, Robert J.
;    APPLICANT:  Lobban, Peter E.
;    APPLICANT:  Morris, Macdonald S.
;    APPLICANT:  Sheldon, Edward L.
;    TITLE OF INVENTION:  Arrays of Nucleic Acid Probes on
;    TITLE OF INVENTION:  Biological Chips
;    NUMBER OF SEQUENCES:  360
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/441,887A
;      FILING DATE:  16-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/143,312
;      FILING DATE:  26-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/082,937
;      FILING DATE:  25-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Liebeschuetz, Joseph O.
;      REGISTRATION NUMBER:  37,505
;      REFERENCE/DOCKET NUMBER:  018547-004160US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-326-2400
;      TELEFAX:  650-326-2422
;  INFORMATION FOR SEQ ID NO:  350:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (probe)
US-08-441-887A-350

  Query Match             100.0%;  Score 6;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+04;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 GGGAGG 6
          ||||||
Db      9 GGGAGG 4


RESULT 12
US-08-441-887A-351/c
; Sequence 351, Application US/08441887A
; Patent No. 5837832
;  GENERAL INFORMATION:
;    APPLICANT:  Chee, Mark
;    APPLICANT:  Cronin, Maureen T.
;    APPLICANT:  Fodor, Stephen P.A.
;    APPLICANT:  Huang, Xiaohua X.
;    APPLICANT:  Hubbell, Earl A.
;    APPLICANT:  Lipshutz, Robert J.
;    APPLICANT:  Lobban, Peter E.
;    APPLICANT:  Morris, Macdonald S.
;    APPLICANT:  Sheldon, Edward L.
;    TITLE OF INVENTION:  Arrays of Nucleic Acid Probes on
;    TITLE OF INVENTION:  Biological Chips
;    NUMBER OF SEQUENCES:  360
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/441,887A
;      FILING DATE:  16-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/143,312
;      FILING DATE:  26-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/082,937
;      FILING DATE:  25-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Liebeschuetz, Joseph O.
;      REGISTRATION NUMBER:  37,505
;      REFERENCE/DOCKET NUMBER:  018547-004160US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-326-2400
;      TELEFAX:  650-326-2422
;  INFORMATION FOR SEQ ID NO:  351:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (probe)
US-08-441-887A-351

  Query Match             100.0%;  Score 6;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+04;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db     10 GGGAGG 5


RESULT 13
US-08-590-571-29
; Sequence 29, Application US/08590571
; Patent No. 5861246
;  GENERAL INFORMATION:
;    APPLICANT:  Sherman Weissman and Girish N. Nallur
;    TITLE OF INVENTION:  MULTIPLE SELECTION PROCESS
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Yahwak & Associates
;      STREET:  25 Skytop Drive
;      CITY:  Trumbull
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06611
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Microsoft Word 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/590,571
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  George M. Yahwak
;      REGISTRATION NUMBER:  26,824
;      REFERENCE/DOCKET NUMBER:  Yale
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203)268-1951
;      TELEFAX:  (203)268-1951
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-590-571-29

  Query Match             100.0%;  Score 6;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+04;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      3 GGGAGG 8


RESULT 14
US-08-906-691-19
; Sequence 19, Application US/08906691
; Patent No. 6066452
;  GENERAL INFORMATION:
;    APPLICANT:  Weissman, Sherman M.
;    APPLICANT:  Nallur, Girish N.
;    APPLICANT:  Kulkarni, Prakash
;    TITLE OF INVENTION:  MULTIPLEX SELECTION TECHNIQUE FOR
;    TITLE OF INVENTION:  IDENTIFYING PROTEIN-BINDING SITES FOR DNA-BINDING PROTEINS
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenu
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  981094
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/906,691
;      FILING DATE:  31-JUL-1997
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;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6066452tenburg Ph.D., Carol
;      REGISTRATION NUMBER:  39,317
;      REFERENCE/DOCKET NUMBER:  390036.403C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-906-691-19

  Query Match             100.0%;  Score 6;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+04;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGAGG 6
           ||||||
Db       3 GGGAGG 8


RESULT 15
PCT-US93-10072-3/c
; Sequence 3, Application PC/TUS9310072
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  "DETECTION OF MITOCHONDRIAL DNA
;    TITLE OF INVENTION:  MUTATIONS
;    TITLE OF INVENTION:  ASSOCIATED WITH ALZHEIMER'S DISEASE AND PARKINSON'S
;    TITLE OF INVENTION:  DISEASE"
;    NUMBER OF SEQUENCES:  3
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 EPO
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/10072
;      FILING DATE:  20-OCT-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/963,723
;      FILING DATE:  20-OCT-1992
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US93-10072-3

  Query Match             100.0%;  Score 6;  DB 5;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+04;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGAGG 6
           ||||||
Db       9 GGGAGG 4


Search completed: October 30, 2002, 09:01:05
Job time : 16.0526 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: October 29, 2002, 07:58:22 ; Search time 68.6316 Seconds
(without alignments)
150.098 Million cell updates/sec

Title: US-09-735-363A-45
Perfect score: 6
Sequence: 1 gggagg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1905168

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
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21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	6	100.0	8	21	AAZ56810	Asub variant oligo
	2	6	100.0	8	21	AAZ56811	Asub variant oligo
	3	6	100.0	8	21	AAZ56812	Asub variant oligo
	4	6	100.0	9	13	AAQ25521	Antisense nucleic
	5	6	100.0	9	18	AAT80306	Oligo HCV-186, tar
c	6	6	100.0	9	18	AAT80313	Oligo HCV-193, tar
c	7	6	100.0	9	19	AAV28792	HCV isolating modu
	8	6	100.0	9	22	AAD15357	Human KCA4 gene ta
	9	6	100.0	10	13	AAQ25520	Antisense nucleic
c	10	6	100.0	10	15	AAQ64610	Alzheimer's/Parkin
c	11	6	100.0	10	15	AAQ79358	Sequence of AP2 re
	12	6	100.0	10	16	AAQ88493	Human mitochondria
	13	6	100.0	10	18	AAT98848	Binding site BSN6
c	14	6	100.0	10	19	AAV35963	Primer used in RAP
	15	6	100.0	10	21	AAC68262	Lama2/APPA transge
	16	6	100.0	10	21	AAC60708	Polynucleotide dir
	17	6	100.0	10	21	AAA61013	Protein binding se
	18	6	100.0	10	21	AAA56520	Human macrophage g
	19	6	100.0	10	21	AAA56547	Human macrophage g
	20	6	100.0	10	21	AAZ61450	Primer SP8F1 for g
c	21	6	100.0	10	21	AAZ77620	Human dendritic ce
c	22	6	100.0	10	21	AAZ77707	Human dendritic ce
	23	6	100.0	10	21	AAZ78095	Human dendritic ce
c	24	6	100.0	10	21	AAZ78160	Human dendritic ce
	25	6	100.0	10	21	AAZ78232	Human dendritic ce
c	26	6	100.0	10	21	AAZ78737	Human dendritic ce
	27	6	100.0	10	21	AAZ78790	Human dendritic ce
	28	6	100.0	10	21	AAZ78869	Human dendritic ce
c	29	6	100.0	10	21	AAZ79049	Human dendritic ce
c	30	6	100.0	10	21	AAZ79339	Human dendritic ce
c	31	6	100.0	10	21	AAZ79354	Human dendritic ce
c	32	6	100.0	10	21	AAZ79555	Human dendritic ce
c	33	6	100.0	10	21	AAZ79748	Human colon prefer
	34	6	100.0	10	21	AAZ79834	Human lung tumour
c	35	6	100.0	10	21	AAZ81223	Metastatic breast
c	36	6	100.0	10	21	AAZ81472	Metastatic breast
c	37	6	100.0	10	21	AAZ81562	Metastatic breast
c	38	6	100.0	10	21	AAZ81588	Metastatic breast
	39	6	100.0	10	21	AAZ81666	Metastatic breast
c	40	6	100.0	10	21	AAZ81824	Metastatic breast
	41	6	100.0	10	21	AAZ81925	Metastatic breast
c	42	6	100.0	10	21	AAZ82099	Metastatic breast
c	43	6	100.0	10	21	AAZ82131	Metastatic breast
	44	6	100.0	10	21	AAZ82177	Metastatic breast
c	45	6	100.0	10	21	AAZ82355	Metastatic breast

ALIGNMENTS

RESULT 1
AAZ56810
ID AAZ56810 standard; DNA; 8 BP.
XX
AC AAZ56810;
XX
DT 25-APR-2000 (first entry)
XX
DE Asub variant oligonucleotide primer P1.
XX
KW Therapeutic; antagonist; high intensity data; HID; HIV-1; integrase;
KW cancer; DNA polymerase; telomerase; aging process; primer; ss.
XX
OS Synthetic.
XX
PN US6017709-A.
XX
PD 25-JAN-2000.
XX
PF 29-APR-1998; 98US-0069434.
XX
PR 29-APR-1998; 98US-0069434.
XX
PA (UYHO-) UNIV HOUSTON.
XX
PI Hardin SH, Jones LB, Ying J;
XX
DR WPI; 2000-136671/12.
XX
PT Screening for therapeutic agents which modulate non-Watson-Crick
PT guanine quartet formation comprises measuring the amount of high
PT intensity data produced by guanine-rich oligonucleotides in the

PT presence of candidate agents -
XX
PS Claim 5; Column 4; 20pp; English.
XX
CC The invention provides a method of screening for potential therapeutic
CC agents which have antagonistic or agonistic activity for the formation
CC of non-Watson-Crick guanine quartets that stabilize higher order guanine
CC -rich oligonucleotide (ON) structures. The method comprises: (a) priming
CC a sequence reaction, in the presence of a test agent, with an ON where
CC the ON forms a non-Watson-Crick structure and produces high intensity
CC data (HID); and (b) measuring the amount of HID production where a
CC decrease in or elimination of the HID is indicative of antagonistic
CC activity, and an increase in the HID is indicative of agonistic
CC activity. The agents could then be used to modulate guanine quartets
CC formations which are involved in HIV-1 integrase inhibition, synapsis
CC formation during meiosis and telomeric maintenance. The method can be
CC modified for determining the susceptibility to cancer by measuring the
CC level of DNA polymerase activity at a quartet stabilized template. The
CC ONs, capable of forming a non-Watson-Crick structure and HID, are used to
CC promote the elongation of telomerases by the action of DNA polymerases
CC and therefore inhibit the aging process. The present sequence represents
CC a guanine-rich oligo that can be used in the method of the invention.
XX
SQ Sequence 8 BP; 2 A; 0 C; 6 G; 0 U; 0 other;

Query Match 100.0%; Score 6; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAGG 6
||||||
Db 3 GGGAGG 8

RESULT 2
AAZ56811
ID AAZ56811 standard; DNA; 8 BP.
XX
AC AAZ56811;
XX
DT 25-APR-2000 (first entry)
XX
DE Asub variant oligonucleotide primer P2.
XX
KW Therapeutic; antagonist; high intensity data; HID; HIV-1; integrase;
KW cancer; DNA polymerase; telomerase; aging process; primer; ss.
XX
OS Synthetic.
XX
PN US6017709-A.
XX
PD 25-JAN-2000.
XX
PF 29-APR-1998; 98US-0069434.
XX
PR 29-APR-1998; 98US-0069434.
XX
PA (UYHO-) UNIV HOUSTON.
XX
PI Hardin SH, Jones LB, Ying J;
XX
DR WPI; 2000-136671/12.
XX
PT Screening for therapeutic agents which modulate non-Watson-Crick
PT guanine quartet formation comprises measuring the amount of high
PT intensity data produced by guanine-rich oligonucleotides in the
PT presence of candidate agents -
XX
PS Claim 5; Column 4; 20pp; English.
XX
CC The invention provides a method of screening for potential therapeutic
CC agents which have antagonistic or agonistic activity for the formation
CC of non-Watson-Crick guanine quartets that stabilize higher order guanine
CC -rich oligonucleotide (ON) structures. The method comprises: (a) priming
CC a sequence reaction, in the presence of a test agent, with an ON where
CC the ON forms a non-Watson-Crick structure and produces high intensity
CC data (HID); and (b) measuring the amount of HID production where a
CC decrease in or elimination of the HID is indicative of antagonistic
CC activity, and an increase in the HID is indicative of agonistic
CC activity. The agents could then be used to modulate guanine quartets
CC formations which are involved in HIV-1 integrase inhibition, synapsis
CC formation during meiosis and telomeric maintenance. The method can be
CC modified for determining the susceptibility to cancer by measuring the
CC level of DNA polymerase activity at a quartet stabilized template. The
CC ONs, capable of forming a non-Watson-Crick structure and HID, are used to
CC promote the elongation of telomerases by the action of DNA polymerases
CC and therefore inhibit the aging process. The present sequence represents
CC a guanine-rich oligo that can be used in the method of the invention.
XX
SQ Sequence 8 BP; 2 A; 0 C; 6 G; 0 U; 0 other;

Query Match 100.0%; Score 6; DB 21; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAGG 6
||||||
Db 2 GGGAGG 7

RESULT 3
AAZ56812
ID AAZ56812 standard; DNA; 8 BP.
XX
AC AAZ56812;
XX
DT 25-APR-2000 (first entry)
XX
DE Asub variant oligonucleotide primer P3.
XX
KW Therapeutic; antagonist; high intensity data; HID; HIV-1; integrase;
KW cancer; DNA polymerase; telomerase; aging process; primer; ss.
XX
OS Synthetic.
XX
PN US6017709-A.
XX
PD 25-JAN-2000.
XX
PF 29-APR-1998; 98US-0069434.
XX
PR 29-APR-1998; 98US-0069434.
XX
PA (UYHO-) UNIV HOUSTON.
XX
PI Hardin SH, Jones LB, Ying J;
XX
DR WPI; 2000-136671/12.
XX
PT Screening for therapeutic agents which modulate non-Watson-Crick
PT guanine quartet formation comprises measuring the amount of high
PT intensity data produced by guanine-rich oligonucleotides in the
PT presence of candidate agents -
XX
PS Claim 5; Column 4; 20pp; English.
XX
CC The invention provides a method of screening for potential therapeutic
CC agents which have antagonistic or agonistic activity for the formation
CC of non-Watson-Crick guanine quartets that stabilize higher order guanine
CC -rich oligonucleotide (ON) structures. The method comprises: (a) priming
CC a sequence reaction, in the presence of a test agent, with an ON where
CC the ON forms a non-Watson-Crick structure and produces high intensity
CC data (HID); and (b) measuring the amount of HID production where a
CC decrease in or elimination of the HID is indicative of antagonistic
CC activity, and an increase in the HID is indicative of agonistic
CC activity. The agents could then be used to modulate guanine quartets

```
CC   formations which are involved in HIV-1 integrase inhibition, synapsis
CC   formation during meiosis and telomeric maintenance. The method can be
CC   modified for determining the susceptibility to cancer by measuring the
CC   level of DNA polymerase activity at a quartet stabilized template. The
CC   ONs, capable of forming a non-Watson-Crick structure and HID, are used to
CC   promote the elongation of telomerases by the action of DNA polymerases
CC   and therefore inhibit the aging process. The present sequence represents
CC   a guanine-rich oligo that can be used in the method of the invention.
XX
SQ   Sequence 8 BP; 2 A; 0 C; 6 G; 0 U; 0 other;

  Query Match          100.0%;  Score 6;  DB 21;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 2e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGAGG 6
           ||||||
Db       1 GGGAGG 6


RESULT 4
AAQ25521
ID   AAQ25521 standard; DNA; 9 BP.
XX
AC   AAQ25521;
XX
DT   01-DEC-1992  (first entry)
XX
DE   Antisense nucleic acid derivative 20.
XX
KW   HIV; ras; c-myb; AIDS-related complex; ss.
XX
OS   Synthetic.
XX
PN   WO9208729-A.
XX
PD   29-MAY-1992.
XX
PF   18-NOV-1991;   91WO-JP01572.
XX
PR   20-NOV-1990;   90JP-0315007.
XX
PA   (SANY ) SANKYO CO LTD.
XX
PI   Furukawa H,  Hotoda H,  Kaneko M,  Momota K,  Takiguchi Y;
XX
DR   WPI; 1992-200131/24.
XX
PT   New antiviral and antitumoural antisense nucleic acid derivs. -
PT   useful for treating AIDS and AIDS-related complex
XX
PS   Claim 79; Page 201; 235pp; Japanese.
XX
CC   The sequences given in AAQ25502-21 are nucleic acid derivatives which
CC   are complementary to either a viral or a tumor gene ie. the sequence
CC   is complementary to the HIV gene at 7947-7975 on the viral genome or
CC   to the ras or c-myb oncogenes.  These derivatives are useful as
CC   anticancer and antiviral agents, esp. for the treatment of AIDS and
CC   AIDS-related complex.  They may be given orally or parenterally.
CC   The derivatives were tritiated so that they could be monitored
CC   easily.
XX
SQ   Sequence 9 BP; 1 A; 0 C; 6 G; 2 T; 0 other;

  Query Match          100.0%;  Score 6;  DB 13;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.8e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGAGG 6
           ||||||
Db       2 GGGAGG 7


RESULT 5
AAT80306
ID   AAT80306 standard; DNA; 9 BP.
XX
AC   AAT80306;
XX
DT   16-OCT-1997  (first entry)
XX
DE   Oligo HCV-186, targetted to HCV mRNA position -216 to -208.
XX
KW   Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW   inhibition; replication; expression; detection; chronic hepatitis;
KW   acute hepatitis; hepatocarcinoma; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1..9
FT                    /*tag=  a
FT                    /note= "Comprises phosphorothioate linkages"
XX
PN   WO9639500-A2.
XX
PD   12-DEC-1996.
XX
PF   04-JUN-1996;   96WO-EP02427.
XX
PR   06-JUN-1995;   95US-0471968.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA   (HYBR-) HYBRIDON INC.
XX
PI   Frank BL,  Goodchild J,  Hamlin HA,  Kilkuskie RE;
PI   Roberts NA,  Roberts PC, Walther DM,  Wolfe JL;
XX
DR   WPI; 1997-043122/04.
XX
PT   Oligo:nucleotide(s) complementary to HCV 5' untranslated region -
PT   used in the treatment and detection of HCV infection, esp. hepatitis
PT   and hepato-carcinoma
XX
PS   Claim 1; Page 17; 100pp; English.
XX
CC   The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC   which are complementary to a portion of the 5' untranslated region (UTR)
CC   of hepatitis C virus (HCV).  These sequences may be used in a
CC   pharmaceutical composition for the control or prevention of HCV
CC   infection. They may be used to inhibit replication or expression of
CC   HCV or for detecting the presence of HCV in a sample.  They may be used
CC   to inhibit HCV replication in a cell and are therefor useful in the
CC   treatment of HCV infections such as chronic and acute hepatitis and
CC   hepatocarcinoma.
XX
SQ   Sequence 9 BP; 1 A; 3 C; 5 G; 0 U; 0 other;

  Query Match          100.0%;  Score 6;  DB 18;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.8e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGAGG 6
           ||||||
Db       4 GGGAGG 9


RESULT 6
AAT80313/c
ID   AAT80313 standard; RNA; 9 BP.
XX
AC   AAT80313;
XX
DT   16-OCT-1997  (first entry)
XX
DE   Oligo HCV-193, targetted to HCV mRNA position -27 to -19.
```

```
XX
KW   Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW   inhibition; replication; expression; detection; chronic hepatitis;
KW   acute hepatitis; hepatocarcinoma; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1..9
FT                   /*tag= a
FT                   /note= "Comprises phosphorothioate linkages"
XX
PN   WO9639500-A2.
XX
PD   12-DEC-1996.
XX
PF   04-JUN-1996;   96WO-EP02427.
XX
PR   06-JUN-1995;   95US-0471968.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA   (HYBR-) HYBRIDON INC.
XX
PI   Frank BL,  Goodchild J,  Hamlin HA,  Kilkuskie RE;
PI   Roberts NA,  Roberts PC, Walther DM,  Wolfe JL;
XX
DR   WPI; 1997-043122/04.
XX
PT   Oligo:nucleotide(s) complementary to HCV 5' untranslated region -
PT   used in the treatment and detection of HCV infection, esp. hepatitis
PT   and hepato-carcinoma
XX
PS   Claim 1; Page 17; 100pp; English.
XX
CC   The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC   which are complementary to a portion of the 5' untranslated region (UTR)
CC   of hepatitis C virus (HCV).  These sequences may be used in a
CC   pharmaceutical composition for the control or prevention of HCV
CC   infection. They may be used to inhibit replication or expression of
CC   HCV or for detecting the presence of HCV in a sample.  They may be used
CC   to inhibit HCV replication in a cell and are therefor useful in the
CC   treatment of HCV infections such as chronic and acute hepatitis and
CC   hepatocarcinoma.
XX
SQ   Sequence 9 BP; 0 A; 5 C; 3 G; 1 U; 0 other;

  Query Match             100.0%;  Score 6;  DB 18;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGAGG 6
           ||||||
Db       6 GGGAGG 1


RESULT 7
AAV28792/c
ID   AAV28792 standard; DNA; 9 BP.
XX
AC   AAV28792;
XX
DT   05-AUG-1998  (first entry)
XX
DE   HCV isolating modular oligonucleotide H1-9.
XX
KW   Hepatitis C virus; HCV; human immunodeficiency virus; HIV; probe;
KW   primer extension product; binding; amplification; primer; detection;
KW   isolation; module; diagnosis; ss.
XX
OS   Synthetic.
OS   Hepatitis C virus.
XX
PN   WO9813522-A1.
XX
PD   02-APR-1998.
XX
PF   26-SEP-1997;   97WO-GB02629.
XX
PR   26-SEP-1996;   96GB-0020075.
XX
PA   (DYNA-) DYNAL AS.
PA   (DZIE/) DZIEGLEWSKA H E.
XX
PI   Lundeberg J,  Uhlen M;
XX
DR   WPI; 1998-230726/20.
XX
PT   Improving binding of series of nucleotide(s) to complementary target
PT   nucleic acid - comprises use of oligo:nucleotide with at least two
PT   modules providing more specific or stable binding, useful in, e.g.
PT   amplification of target
XX
PS   Claim 17; Page 52; 71pp; English.
XX
CC   A method has been developed for improving the binding of a series of
CC   consecutive nucleotides (nt) to a complementary target nucleic acid in
CC   a sample. The method comprises binding a complementary modular
CC   oligonucleotide, having at least 2 parts comprising nt, to adjacent
CC   stretches of the target nucleic acid. The complementary modular
CC   oligonucleotide has better binding than a single oligonucleotide
CC   complementary to the region spanned by the complementary modular
CC   oligonucleotide. The present sequence represents a specifically claimed
CC   component of a complementary modular oligonucleotide. The complementary
CC   modular oligonucleotides are used as probes or primers, for replication,
CC   amplification, (reverse) transcription, sequencing, isolation and/or
CC   detection of the target nucleic acid. Specific applications are
CC   detection/isolation of hepatitis C virus (HCV), human immunodeficiency
CC   virus (HIV), e.g. for diagnosis or monitoring of infections, or
CC   (universal) primer extension products, e.g. before electrophoretic
CC   separation. Use of the complementary modular oligonucleotides improves
CC   binding specificity, stability or ability (probably by disrupting the
CC   tertiary structure of the target nucleic acid) and the method is
CC   suitable for automation since pre-hybridisation, sample lysis and bead
CC   capture can be combined in a single step.
XX
SQ   Sequence 9 BP; 0 A; 5 C; 3 G; 1 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 19;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+08;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGAGG 6
           ||||||
Db       6 GGGAGG 1


RESULT 8
AAD15357
ID   AAD15357 standard; DNA; 9 BP.
XX
AC   AAD15357;
XX
DT   15-NOV-2001  (first entry)
XX
DE   Human KCA4 gene target sequence.
XX
KW   Human; KCA4; EPO; molecular target; zinc finger protein; ZFP;
KW   cellular process; signal transduction; drug-screening; ds.
XX
OS   Homo sapiens.
XX
PN   WO200159450-A2.
XX
PD   16-AUG-2001.
XX
PF   08-FEB-2001; 2001WO-US04301.
```

XX
PR 08-FEB-2000; 2000US-0181117.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Case C;
XX
DR WPI; 2001-522491/57.
XX
PT Screening compound for interaction with molecular target by contacting
PT compound with cells, comprising exogenous zinc finger protein that
PT modulates expression of target, and determining values of properties of
PT cells -
XX
PS Example 10; Page 73; 99pp; English.
XX
CC The invention relates to a method of screening a compound for interaction
CC with a molecular target. The method involves contacting first and
CC second cells with the compound and determining the values of properties
CC of the compound. The second cell comprises an exogenous zinc finger
CC protein (ZFP) that modulates the expression of the molecular target, or
CC isolating membranes from cell comprising ZFP. The methods allow for high
CC throughput screening of candidate compound and reduces the incidence of
CC false positives. The methods are useful for screening a compound for
CC interaction with a molecular target or for screening a compound for its
CC effect on a cellular process. The method is useful for testing a compound
CC for its capacity to transduce a signal to the molecular target or its
CC capacity to block transduction of a signal through the molecular target,
CC and for performing biochemical drug-screening assays. The present
CC sequence is a target sequence for human KCa4 gene used in the
CC exemplification of the invention.
XX
SQ Sequence 9 BP; 1 A; 1 C; 7 G; 0 U; 0 other;

Query Match 100.0%; Score 6; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAGG 6
||||||
Db 2 GGGAGG 7

RESULT 9
AAQ25520
ID AAQ25520 standard; DNA; 10 BP.
XX
AC AAQ25520;
XX
DT 01-DEC-1992 (first entry)
XX
DE Antisense nucleic acid derivative 19.
XX
KW HIV; ras; c-myb; AIDS-related complex; ss.
XX
OS Synthetic.
XX
PN WO9208729-A.
XX
PD 29-MAY-1992.
XX
PF 18-NOV-1991; 91WO-JP01572.
XX
PR 20-NOV-1990; 90JP-0315007.
XX
PA (SANY) SANKYO CO LTD.
XX
PI Furukawa H, Hotoda H, Kaneko M, Momota K, Takiguchi Y;
XX
DR WPI; 1992-200131/24.
XX
PT New antiviral and antitumoural antisense nucleic acid derivs. -
PT useful for treating AIDS and AIDS-related complex
XX
PS Claim 78; Page 200; 235pp; Japanese.
XX
CC The sequences given in AAQ25502-21 are nucleic acid derivatives which
CC are complementary to either a viral or a tumor gene ie. the sequence
CC is complementary to the HIV gene at 7947-7975 on the viral genome or
CC to the ras or c-myb oncogenes. These derivatives are useful as
CC anticancer and antiviral agents, esp. for the treatment of AIDS and
CC AIDS-related complex. They may be given orally or parenterally.
CC The derivatives were tritiated so that they could be monitored
CC easily.
XX
SQ Sequence 10 BP; 1 A; 0 C; 7 G; 2 T; 0 other;

Query Match 100.0%; Score 6; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAGG 6
||||||
Db 2 GGGAGG 7

RESULT 10
AAQ64610/c
ID AAQ64610 standard; cDNA; 10 BP.
XX
AC AAQ64610;
XX
DT 15-DEC-1994 (first entry)
XX
DE Alzheimer's/Parkinsons mitochondrial DNA mutation detection.
XX
KW Mitochondrial DNA mutation; associated with Alzheimer's;
KW Parkinson's disease; mismatch primers; PCR; amplification;
KW polymerase chain reaction; ss.
XX
OS Homo sapiens.
XX
PN WO9409162-A.
XX
PD 28-APR-1994.
XX
PF 20-OCT-1993; 93WO-US10072.
XX
PR 20-OCT-1992; 92US-0963723.
XX
PA (UYEM-) UNIV EMORY SCHOOL MEDICINE.
XX
PI Wallace DC;
XX
DR WPI; 1994-151346/18.
XX
PT Detection of mitochondrial DNA mutation associated with
PT Alzheimer's disease and/or Parkinson's disease - for diagnosing
PT or predicting a pre-disposition to Alzheimer's disease and/or
PT Parkinson's disease in a patient
XX
PS Disclosure; Page 36; 83pp; English.
XX
CC A 12S(956-965) insertion mutation harbours a novel 12S rRNA gene
CC insertion. Direct sequence analysis revealed that the insertion
CC consisted of approximately five cytosines within AAQ64610.
CC This mitochondrial DNA mutation is associated with Alzheimer's
CC and/or Parkinson's diseases. The detection of the mutations is
CC useful for diagnosing or predicting a pre-disposition to either
CC of the diseases.
XX
SQ Sequence 10 BP; 0 A; 9 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 6; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GGGAGG 6
          ||||||
Db      9 GGGAGG 4


RESULT 11
AAQ79358/c
ID   AAQ79358 standard; DNA; 10 BP.
XX
AC   AAQ79358;
XX
DT   05-JUN-1995  (first entry)
XX
DE   Sequence of AP2 regulatory sequence located at posn. 896 in
DE   hEpSLH.
XX
KW   Erythropoietin; erythropoiesis; red blood cell; regulatory element;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO9423570-A.
XX
PD   27-OCT-1994.
XX
PF   15-APR-1994;   94WO-US04141.
XX
PR   15-APR-1993;   93US-0046295.
PR   23-JUN-1993;   93US-0082850.
XX
PA   (UYNY ) UNIV NEW YORK STATE.
XX
PI   Lee-huang S;
XX
DR   WPI; 1994-341353/42.
XX
PT   New regulatory regions of human erythropoietin gene - used for
PT   studying and treating diseases and for prodn. of transgenic
PT   animal models.
XX
PS   Disclosure; Table I, p. 12; 81pp; English.
XX
CC   AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone
CC   hEpSLH. This nucleic acid sequence includes EPO coding sequence, a 5'
CC   flanking region contg. multiple regulatory elements and a 3'
CC   flanking region contg. multiple regulatory elements. AAQ79354 shows
CC   the extended 5' flanking region and includes all the 5' regulatory
CC   elements. This region, consisting of the first 3892 of AAQ79353, was
CC   not found in the 3.6 kb EPO genomic clone from fetal liver reported
CC   by others. The flanking region comprises 3892 bp and contains
CC   CAAT and TATA boxes and at lease 321 potential transcriptional
CC   regulatory elements. AAQ79356-Q79362 show several of these elements
CC   and their positions. The nucleotide position of these elements is
CC   measured from the BamHI site at the 5' end of AAQ79353.
XX
SQ   Sequence 10 BP; 0 A; 8 C; 0 G; 2 T; 0 other;

  Query Match             100.0%;  Score 6;  DB 15;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db     10 GGGAGG 5


RESULT 12
AAQ88493
ID   AAQ88493 standard; DNA; 10 BP.
XX
AC   AAQ88493;
XX
DT   20-DEC-1995  (first entry)
XX
DE   Human mitochondrial D-loop region DNA probe 4-4.
XX
KW   Tiling strategy; immobilised nucleic acid probe array;
KW   mitochondrial DNA; D-loop region; biological chip;
KW   hybridisation fingerprint; interrogation position; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   10
FT                   /*tag= a
FT                   /note= "3'-end of probe is covalently attached
FT                          to chip surface"
XX
PN   WO9511995-A1.
XX
PD   04-MAY-1995.
XX
PF   26-OCT-1994;   94WO-US12305.
XX
PR   02-AUG-1994;   94US-0284064.
PR   26-OCT-1993;   93US-0143312.
XX
PA   (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX
PI   Chee M,  Cronin MT,  Fodor SPA,  Gingeras TR,  Huang XC;
PI   Hubbell EA, Lipshutz RJ,  Lobban PE,  Miyada CG,  Morris MS;
PI   Shah N,  Sheldon EL;
XX
DR   WPI; 1995-178887/23.
XX
PT   New arrays of oligo:nucleotide probes - used for comparing known
PT   sequences with variants for detection of mutation(s) and sequencing.
XX
PS   Disclosure; Page 107; 223pp; English.
XX
CC   A DNA chip was prepared for analysing sequences contained in a
CC   1.3kb fragment of human mitochondrial DNA from the D-loop region,
CC   the most polymorphic region of human mitochondrial DNA. The chip
CC   comprised a set of 268 overlapping oligonucleotide probes (see
CC   AAQ88421-Q88684) of varying length (9-14 nucleotides) with varying
CC   overlaps arranged in a 1cm x 1cm array. Each position in the
CC   sequence was represented by at least one probe (usually 2 or more).
CC   DNA was amplified from six human donors and then transcribed to
CC   give the 1.3kb RNA transcripts which were fragmented and hybridised
CC   to the chip. For each individual, a unique hybridisation fingerprint
CC   was produced on the chip; all differences could be correlated with
CC   differences in the cloned genomic DNA sequence.
XX
SQ   Sequence 10 BP; 1 A; 1 C; 8 G; 0 U; 0 other;

  Query Match             100.0%;  Score 6;  DB 16;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGAGG 6
          ||||||
Db      5 GGGAGG 10


RESULT 13
AAT98848
ID   AAT98848 standard; DNA; 10 BP.
XX
AC   AAT98848;
XX
DT   20-MAR-1998  (first entry)
XX
DE   Binding site BSN6 identified using the method of the invention.
XX
KW   Protein-binding site isolation; transcription factor modification;
```

KW DNA-binding protein; inhibitor identification; ss.
XX
OS Synthetic.
XX
PN WO9727330-A1.
XX
PD 31-JUL-1997.
XX
PF 24-JAN-1997; 97WO-US01230.
XX
PR 24-JAN-1996; 96US-0590571.
XX
PA (UYYA) UNIV YALE.
XX
PI Kulkarni P, Nallur GN, Weissman SM;
XX
DR WPI; 1997-393714/36.
XX
PT Identifying protein-binding sites for DNA-binding proteins - using
PT duplexes having 5' and 3' sequences for annealing to amplification
PT primers with an internal potential protein-binding site sequence
XX
PS Example 3; Page 19; 52pp; English.
XX
CC This sequence represents a binding site identified using the method of
CC the invention. This sequence was identified using the 32P-labelled
CC oligonucleotide duplex shown in AAT76581 and the primers shown in
CC AAT76582-T76583 in the method of the invention. The method is for
CC simultaneously isolating protein-binding sites for DNA-binding proteins.
CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes
CC having 5' and 3' sequences capable of annealing to primers for
CC amplification and an internal sequence having a potential
CC protein-binding site, a non-specific inhibitor and a sample containing
CC DNA-binding proteins; (b) separating unbound ON duplexes from ON duplexes
CC complexed with the DNA-binding proteins; (c) amplifying complexed
CC duplexes to form amplified duplexes; thereby isolating protein-binding
CC sites for the DNA-binding proteins. The methods can be used to identify
CC protein-binding sites which can be used to identify corresponding
CC DNA-binding proteins in an expression library. They can also be used to
CC develop products to inhibit the function of a given DNA-binding protein
CC or for the modification of transcription factors.
XX
SQ Sequence 10 BP; 1 A; 0 C; 7 G; 2 T; 0 other;

Query Match 100.0%; Score 6; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAGG 6
||||||
Db 3 GGGAGG 8

RESULT 14
AAV35963/c
ID AAV35963 standard; DNA; 10 BP.
XX
AC AAV35963;
XX
DT 26-AUG-1998 (first entry)
XX
DE Primer used in RAPD assay of the invention.
XX
KW Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;
KW muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.
XX
OS Synthetic.
OS Sus sp.
XX
PN WO9815837-A1.
XX
PD 16-APR-1998.
XX
PF 07-OCT-1997; 97WO-GB02741.
XX
PR 09-SEP-1997; 97GB-0019002.
PR 07-OCT-1996; 96GB-0020904.
PR 18-FEB-1997; 97GB-0003350.
PR 20-MAR-1997; 97GB-0005796.
XX
PA (MEAT-) MEAT & LIVESTOCK COMMISSION.
XX
PI Maltin CA, Steven J, Warkup CC;
XX
DR WPI; 1998-240968/21.
XX
PT Assay for alleles or muscle fibre composition characteristic of
PT Duroc type pigs - comprises determination of genotype or muscle
PT fibre properties, used to identify animals for breeding programs and
PT to assess meat quality
XX
PS Example 3; Page 33; 56pp; English.
XX
CC PCR primers AAV35877-996 were used in a rapid amplification of
CC polymorphic DNA (RAPD) reaction in the assay of the invention. This assay
CC is used to determine if an animal has an allele for, or muscle fibre
CC composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce
CC meat of superior quality (particularly tenderness) but are normally less
CC efficient feed converters and fatter than other types. The assay
CC comprises analysing a tissue sample to determine if the genotype
CC comprises the allele, and genetic features typical of animals with
CC Duroc-type MFC are present. The method is used to select animals that
CC have Duroc characteristics for use in breeding programmes (to develop
CC the animals with Duroc pig characteristics), and to assess meat quality.
XX
SQ Sequence 10 BP; 1 A; 7 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 6; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAGG 6
||||||
Db 10 GGGAGG 5

RESULT 15
AAC68262
ID AAC68262 standard; DNA; 10 BP.
XX
AC AAC68262;
XX
DT 20-FEB-2001 (first entry)
XX
DE Lama2/APPA transgene adaptor sequence #1.
XX
KW Transgenic animal; salivary protein; phytase; phosphorus; animal growth;
KW environmental pollution; pig; ds.
XX
OS Synthetic.
XX
PN WO200064247-A1.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-CA00430.
XX
PR 23-APR-1999; 99US-0130508.
XX
PA (UYGU-) UNIV GUELPH.
XX
PI Forsberg CW, Golovan S, Phillips JP;
XX
DR WPI; 2000-687245/67.
XX
PT Transgenic non-human animal for gastrointestinal tract specific

PT expression of a protein, preferably phytase, comprises a nucleic acid
PT sequence including a heterologous transgene construct encoding the
PT protein -
XX
PS Disclosure; Page 19; 152pp; English.
XX
CC The present invention provides transgenic animals which produce desired
CC proteins, in this case pigs which expresses phytase in the salivary
CC gland. Low phytase production levels result in phytate in the diet being
CC excreted and causing phosphorus contamination in water, as well as
CC reducing the growth of animals. The invention provides a number of
CC transgenes containing the E. coli APPA phytase coding sequence.
XX
SQ Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 other;

Query Match 100.0%; Score 6; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GGGAGG 6
          ||||||
Db      2 GGGAGG 7
```

Search completed: October 29, 2002, 09:11:33
Job time : 68.6316 secs